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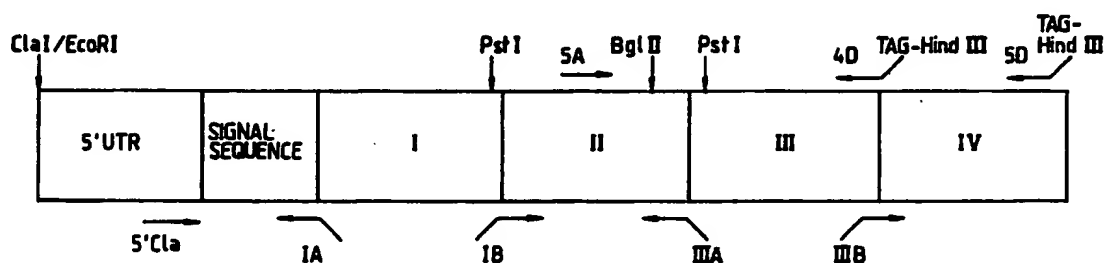
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(54) Title: **MODIFIED HUMAN TNFALPHA (TUMOR NECROSIS FACTOR ALPHA) RECEPTOR**

(57) Abstract

A polypeptide which is capable of binding human TNF α and which consists essentially of: a) the first three cysteine-rich subdomains, but not the fourth cysteine-rich subdomain, of the extracellular binding domain of the 55kD or 75kD receptor for human TNF α ; or b) an amino acid sequence having a homology of 90 % or more with the said sequence (a).

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Modified human TNF α (Tumor Necrosis Factor alpha) Receptor.

The present invention relates to recombinant proteins and their use.

Tumour necrosis factor- α (TNF α) is a potent cytokine which elicits a broad spectrum of biological responses. TNF α causes the cytolysis or cytostasis of many tumour cell lines in vitro, induces the haemorrhagic necrosis of transplanted tumours in mice, enhances the phagocytosis and cytotoxicity of polymorphonuclear neutrophils, and modulates the expression of many proteins, including lipoprotein lipase, class I antigens of the major histocompatibility complex, and cytokines such as interleukin 1 and interleukin 6. TNF α appears to be necessary for a normal immune response, but large quantities produce dramatic pathogenic effects. TNF α has been termed "cachectin" since it is the predominant factor responsible for the wasting syndrome (cachexia) associated with neoplastic disease and parasitemia. TNF is also a major contributor to toxicity in gram-negative sepsis, since antibodies against TNF can protect infected animals.

The many activities of TNF α are mediated by binding to a cell surface receptor. Radioligand binding studies have confirmed the presence of TNF receptors on a wide variety of cell types. Although these receptors are expressed in limited numbers (1,000 - 10,000 receptors/cell), they bind TNF α with high affinity ($K_a = 10^9 M^{-1}$ at 4°C). Lymphotoxin (LT, also termed TNF β) has similar, if not identical, biological activities to TNF α , presumably because both are recognized by the same receptor.

Recently, several laboratories have detected heterogeneity in TNF receptor preparations. Two distinct cell surface receptors which bind TNF α and TNF β have recently been characterised at the molecular level. cDNA for one form of the receptor with a Mr of 55kD was isolated utilising probes designed from the peptide sequence of a

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soluble form of the receptor (1,2). A second receptor of Mr 75kD was cloned by a COS cell expression approach (3). Both receptors are members of a larger family of cytokine receptors which include the nerve growth factor receptor, the B cell antigen CD40, the rat T cell antigen MRC OX40. In addition these receptors are homologous to the predicted product of a transcriptionally active open reading frame from Shope fibroma virus which appears to give rise to a secreted protein.

10 The most conserved feature amongst this group of cell surface receptors is the cysteine rich extracellular ligand binding domain, which can be divided into four repeating motifs of about forty amino acids. We have now generated four soluble receptor derivatives of the 55kD TNF α receptor (TNFR). Each derivative is composed of the extracellular binding domain but without one of the cysteine rich subdomains. We have found that the derivative which lacks the membrane-proximal fourth subdomain retains the ability to bind TNF α with high affinity. This finding has general applicability.

Accordingly, the present invention provides a polypeptide which is capable of binding human TNF α and which consists essentially of:

- (a) the first three cysteine-rich subdomains, but not the fourth cysteine-rich subdomain, of the extracellular binding domain of the 55kD or 75kD receptor for human TNF α ;
or
(b) an amino acid sequence having a homology of 90% or more with the said sequence (a).

30 The invention also provides:

- a DNA sequence which encodes such a polypeptide;
- a vector which incorporates a DNA sequence of the invention and which is capable, when provided in a transformed host, of expressing the polypeptide of the invention encoded by the DNA sequence; and

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a host transformed with such a vector.

In the accompanying drawings:

Figure 1 shows the nucleotide sequence of the human TNF α cDNA and encoded amino acid sequence. The predicted signal sequence residues are numbered -40 to -1. The transmembrane domain is boxed and potential N-linked glycosylation sites are overlined. The sequence homologous with the designed oligonucleotide probe is found at nucleotide positions 477-533.

Figure 2 is a Northern blot (lanes 1-3) of 10 μ g of oligo-dT selected RNA from human 293 cells (fibroblast cell line) (lane 1), placenta (lane 2) and spleen (lane 3) hybridised with the TNF receptor cDNA (SmaI-EcoRI fragment). The Southern blot (lanes 4-6) was hybridized with the same probe. Human genomic DNA (5 μ g per lane) was digested with PstI (lane 4), Hind III (lane 5) and EcoRI (lane 6).

Figure 3 shows the binding characteristics of recombinant human TNF receptor expressed in COS-7 cells. The direct binding of recombinant ¹²⁵I-TNF α to COS-7 cells transfected with pRTNFR is presented in panel A. The inset contains Scatchard analysis derived from this data. As shown in panel B, monolayers of Cos-7 cells transfected with TNFR cDNA were incubated with 1nM ¹²⁵I-TNF in the presence of various concentrations of unlabelled TNF α or TNF β .

Figure 4 shows the effects of soluble TNFR on TNF α binding and biological activity. Panel A shows the effects of supernatants from Cos-7 cells transfected with a cDNA encoding a soluble form of the TNF receptor (pTNFR α cd, closed circles) or mock transfected (open circles) on ¹²⁵I-TNF binding to U937 cells. Panel B shows the effects of these supernatants on TNF mediated killing of WEHI 164 (clone 13) line. Assays were performed as described in Materials and Methods.

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Figure 5 is a diagram of the DNA sequence of pTNFR cd and is also a strategy map for polymerase chain reaction (PCR)-based domain deletion, in which 5'UTR is the 5'-untranslated region and I to IV are the four cysteine-rich subdomains. The oligonucleotides employed in PCR in the Example and relevant restriction sites are also shown.

Figure 6 shows lined up the amino acid sequences of the four cysteine-rich subdomains of the 55kD (TNFR-55) and 75kD (TNFR-75) receptors and of rat nerve growth factor receptor (NGFR), human CD40 and rat OX40. Homology is shown by means of boxes.

Figures 7 to 11 show the nucleotide sequence and the predicted amino acid sequence of the encoded polypeptide of pTNFRecd, p Δ I, p Δ II, p Δ III and p Δ IV.

Figure 12 shows the results of the assays described in the Example 1.

Figure 13 shows diagrammatically the DNA encoding the 75kD receptor in which I to IV are the four cysteine-rich subdomains. Oligonucleotides employed in PCR-domain deletion are also shown.

A polypeptide according to the invention is capable of binding human TNF α . Typically the polypeptide has a binding affinity for human TNF α of 10^7M^{-1} or greater, for example 10^8M^{-1} or greater. The affinity may be from 10^7 to 10^{10}M^{-1} , for example from 10^8 to 10^9M^{-1} .

A preferred polypeptide consists essentially of the first three cysteine-rich subdomains of the extracellular binding domain of the 55kD receptor for human TNF α . The sequence (a₁) of these three subdomains is:

	V	C	P	Q	G															
30	K	Y	I	H	P	Q	N	N	S	I	C	C	T	K	C	H	K	G	T	Y
	L	Y	N	D	C	P	G	P	G	Q	D	T	D	C	R	E	C	E	S	G
	S	F	T	A	S	E	N	H	L	R	H	C	L	S	C	S	K	C	R	K
	E	M	G	Q	V	E	I	S	S	C	T	V	D	R	D	T	V	C	G	C
	R	K	N	Q	Y	R	H	Y	W	S	E	N	L	F	Q	C	F	N	C	S
35	L	C	L	N	G	T	V	H	L	S	C	Q	E	K	Q	N	T	V	C	

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A useful polypeptide has the amino acid sequence (c):

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M G L S T V P D L L L P L V L L E L L V
G I Y P S G V I G L V P H L G D R E K R
D S V C P Q G K Y I H P Q N N S I C C T
5 K C H K G T Y L Y N D C P G P G Q D T D
C R E C E S G S F T A S E N H L R H C L
S C S K C R K E M G Q V E I S S C T V D
R D T V C G C R K N Q Y R H Y W S E N L
F Q C F N C S L C L N G T V H L S C Q E
10 K Q N T V C T.

```

In an alternative embodiment, the polypeptide may consist essentially of the first three cysteine-rich subdomains of the extracellular binding domain of the 75kD receptor.

15 Apart from the amino acid sequence (a), the polypeptides may alternatively consist essentially of an amino acid sequence (b) having a homology of 90% or more with sequence (a). The degree of homology may be 95% or more or 98% or more. Amino acid sequence (a) may therefore be modified by
 20 one or more amino acid substitutions, insertions and/or deletions and/or by an extension at either or each end. There should be no modification of the cysteine-residues, however. A polypeptide comprising sequence (b) must of course still be capable of binding human TNF α .

25 For example, one or more amino acid residues of the sequence (a), other than a cysteine residue, may be substituted or deleted or one or more additional amino acid residues may be inserted; provided the physicochemical character of the original sequence is preserved, i.e. in
 30 terms of charge density, hydrophobicity/hydrophilicity, size and configuration. Conservative substitutions may be made. Candidate substitutions are, based on the one-letter code (Eur. J. Biochem. 138, 9-37, 1984):

35 A for G and vice versa,

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V by A, L or G;

K by R;

S by T and vice versa;

E for D and vice versa; and

5 Q by N and vice versa.

Up to 15 residues may be deleted from the N-terminal and/or C-terminal of the polypeptide, for example up to 11 residues or up to 5 residues.

The polypeptides of the invention consist essentially of
 10 sequence (a) or (b). They do not contain a fourth cysteine-rich subdomain. However, the polypeptides may be longer polypeptides of which sequence (a) or (b) is a part. A short sequence of up to 50 amino acid residues may be provided at either or each terminal of sequence (a) or (b).
 15 The sequence may have up to 30, for example up to 20 or up to 10, amino acid residues.

Alternatively, a much longer extension may be present at either or each terminal of sequence (a) or (b) of up to, for example, 100 or 200 amino acid residues. Longer amino
 20 acid sequences may be fused to either or each end. A chimaeric protein may be provided in which the or each extension is a heterologous amino acid sequence, i.e. a sequence not naturally linked to the amino acid sequence above. Such a chimaeric protein may therefore combine the
 25 ability to bind specifically to human TNF α with another functionality.

The polypeptides of the invention lack the fourth cysteine-rich subdomain of the 55kD or 75kD receptor as the case may be. In particular, they lack the cysteine
 30 residues of the fourth subdomain. They therefore do not comprise, immediately after the third cysteine-rich subdomain, any of the amino acid sequence up to the last cysteine residue of the fourth cysteine-rich subdomain of the r levant r cept r except p ssibly the first amino acid
 35 residue f that s quence. The p lypeptides may extend

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beyond that first amino acid residue as indicated above, though, by way of their amino acid sequences.

The polypeptides are typically recombinant polypeptides, although they may be made by synthetic methods such as

5 solid-phase or solution-phase polypeptide synthesis in which case an automated peptide synthesiser may be employed. They may therefore commence with a N-terminal residue M. They are prepared by recombinant DNA technology. The preparation of the polypeptides therefore

10 depends upon the provision of a DNA sequence encoding the polypeptide. A suitable sequence encoding the first three cysteine-rich subdomains of the extracellular binding domain of the 55kD receptor comprises: GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC AAG TGC

15 CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG AGT

20 GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC.

A DNA sequence may further comprise a DNA sequence encoding a signal sequence fused to the 5' end of the coding sequence. Any signal sequence may be appropriate.

25 The signal sequence should be capable of directing secretion of the polypeptide of the invention from the cell in which the polypeptide is expressed. The signal sequence may be the natural signal sequence for the 55kD TNF α receptor. An appropriate DNA sequence encoding the first

30 three cysteine-rich subdomains of the extracellular binding domain of the 55kD receptor and such a signal sequence is therefore: ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCG CTG GTG CTC CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT

35 GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT

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TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT
CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC
TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC
TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC
5 ACA GTG GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC
CGG CAT TAT TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC
CTC TGC CTC AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG
AAC ACC GTG TGC ACC.

A DNA sequence encoding a polypeptide of the invention
10 may be synthesised. Alternatively, it may be constructed
by isolating a DNA sequence encoding the 55kD or 75kD
receptor from a gene library and deleting DNA downstream of
the coding sequence for the first three cysteine-rich
subdomains of the extracellular binding domain of the
15 receptor. This gives DNA encoding the first three
subdomains of either receptor. As an intermediate step,
DNA encoding the entire or nearly the entire extracellular
binding domain may be isolated and digested to remove DNA
downstream of the coding sequence for the first three
20 subdomains.

A modified nucleotide sequence, for example encoding an
amino acid sequence (b), may be obtained by use of any
appropriate technique, including restriction with an
endonuclease, insertion of linkers, use of an exonuclease
25 and/or a polymerase and site-directed mutagenesis. Whether
a modified DNA sequence encodes a polypeptide of the
invention can be readily ascertained. The polypeptide
encoded by the sequence can be expressed in a suitable host
and tested for its ability to bind specifically human TNF α .

30 For expression of a polypeptide of the invention, an
expression vector is constructed. An expression vector is
prepared which comprises a DNA sequence encoding a
polypeptide of the invention and which is capable of
expressing the polypeptide when provided in a suitable
35 host. Appropriate transcriptional and translational

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control elements are provided, including a promoter for the DNA sequence, a transcriptional termination site, and translational start and stop codons. The DNA sequence is provided in the correct frame such as to enable expression of the polypeptide to occur in a host compatible with the vector.

The expression vector is then provided in an appropriate host. Cells harbouring the vector are grown so as to enable expression to occur. The vector may be a plasmid or a viral vector. Any appropriate host-vector system may be employed.

The transformed host may be a prokaryotic or eukaryotic host. A bacterial or yeast host may be employed, for example E. coli or S. cerevisiae. Insect cells can alternatively be used, in which case a baculovirus expression system may be appropriate. As a further alternative, cells of a mammalian cell line, such as Chinese Hamster Ovary (CHO) Cells may be transformed. A polypeptide glycosylated at one, two or three of the sites shown in Figure 1 can be obtained by suitable choice of the host cell culture.

The polypeptide of the invention can be isolated and purified. The N-terminal of the polypeptide may be heterogeneous due to processing of the translation product within a cell or as the product is being secreted from a cell. A mixture of polypeptides according to the invention, having different N-termini, may therefore be obtained. The polypeptide is soluble.

The polypeptides of the invention have activity binding human TNF α . This activity is indicative of the possible use of the polypeptides in the regulation of TNF α -mediated responses by binding and sequestering human TNF α , for example possible use in treatment of pulmonary diseases, septic shock, HIV infection, malaria, viral meningitis, graft versus host reactions and autoimmune diseases such as

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rheumat id arthritis.

For this purpose, a polypeptide of the present invention may be formulated in a pharmaceutical composition. The pharmaceutical composition also comprises a
5 pharmaceutically acceptable carrier or diluent.

The polypeptide of the invention may be administered to a patient by any convenient route. The choice of whether an oral route or a parenteral route, such as subcutaneous, intravenous or intramuscular administration, is adopted; of
10 the dose; and of the frequency of administration depends upon a variety of factors. These factors include the purpose of the administration, the age and weight of the patient being treated and the condition of the patient. Typically, however, the polypeptide is administered in an
15 amount of from 1 to 1000 μ g per dose, more preferably from 10 to 100 μ g per dose, for each route of administration.

The following Examples illustrate the invention. A Reference Example is provided.

REFERENCE EXAMPLE

20 1. Materials and Methods

Reagents

Recombinant human TNF α and TNF β were supplied as highly purified proteins derived from *E. coli*. The specific activities of these preparations were approximately 10⁷
25 units/mg, as measured in the murine L929 cell cytotoxicity assay (4). The synthetic oligonucleotides were prepared by Oswel DNA Service (University of Edinburgh).

Isolation of TNF α 55kD receptor cDNA clones

The sequence of a peptide fragment (E M G Q V E I S S T
30 V D R D T V C G) of the TNF binding protein was used to design a synthetic oligonucleotide probe (5' AAG GAG ATG GGC CAG GTT GAG ATC TCT TCT ACT GTT GAC AAT GAC ACT GTG TGT GGC-3'). The 57-mer DNA probe was labelled with ³²P and T4

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- polynucleotide kinase (New England Biolabs, Beverly, MA) and used to screen a placenta cDNA library in gt10 (5,6). Approximately 800,000 phage were transferred to nitrocellulose filters and screened at reduced stringency
- 5 (7). Filters were incubated for 2 hours at 42°C in 0.05M sodium phosphate, pH 6.5, 20% formamide, 0.75 M sodium chloride, 0.075 M sodium citrate, 1% polyvinyl pyrrolidone (Sigma, St Louis, MO), 1% Ficoll, 1% bovine serum albumin (Sigma), and 50 ng/ml sonicated salmon sperm DNA (Sigma).
- 10 The radiolabelled probe was then added to the filters (10^8 cpm/ml final concentration) which were hybridized for 16 hours. Filters were washed extensively in 0.06M sodium chloride, 0.006M sodium citrate, 1% SDS at 37°C and positive clones were identified by autoradiography. Ten
- 15 hybridizing clones were plaque purified (5) and cDNA insert size was determined by polyacrylamide gel electrophoresis of EcoRI digested phage DNA. The inserts of two cDNA clones were sequenced using the dideoxy chain termination technique (8).
- 20 Southern and Northern blot analysis
- DNA was isolated from human lymphocytes by the method of Blin and Stafford (9) and used for Southern blot analysis (10). DNA was digested with restriction endonucleases (New England Biolabs), fractionated on a 1% agarose gel, and
- 25 transferred to nitrocellulose. Hybridization and washing were conducted under stringent conditions (6) using a ^{32}P -labelled preparation of a 600 bp fragment of the TNF receptor cDNA. Northern blot analysis was performed (11) on oligo-dT selected RNA isolated from human placenta,
- 30 spleen (generously provided by the Cooperative Human Tissue Network, Birmingham, AL) and a fibroblast cell line (293 cells). Following electrophoresis on a formaldehyde 1.2% agarose gel, the RNA was transferred to nitrocellulose and hybridized with the TNF α receptor DNA probe under stringent
- 35 conditions.

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Mammalian cell expression of the human TNF α 55kD
receptor and derivatives

The coding region of the majority of the human TNF α 55kD receptor was isolated as an EcoRI fragment and cloned into a mammalian cell expression vector (12), resulting in plasmid prTNFR. The EcoRI fragment encodes 374 amino acids of the TNF receptor; the 81 carboxyl terminal residues of the cytoplasmic domain are therefore missing from this plasmid construction. A derivative of the TNF α receptor was produced by engineering a termination codon just prior to the transmembrane domain. The polymerase chain reaction (PCR) technique (13) was used to generate a 300 bp restriction fragment containing a BgIII site at the 5' end and a HindIII site preceded by a TAG stop codon at the 3' end. The PCR primers were 5'-GCTGCTCCAAATGCCGAAAG and 5'-AGTTC AAGCTTTTACAGTGCCCTTAACATTCTAA.

The PCR product was gel purified and cloned into the TNF receptor expression plasmid (described above) digested with BgIII and HindIII. DNA sequencing confirmed that the resulting plasmid (pTNFREcd) contained the designed DNA sequence. *E. coli* harbouring pTNFREcd were deposited at the National Collection of Industrial and Marine Bacteria, Aberdeen, GB on 11 September 1990 under accession number NCIMB 40315.

The TNF α receptor expression plasmids were transfected into monkey COS-7 cells using Lipofectin (Gibco BRL, Bethesda, MD) according to the manufacturer's instructions. Cells were cultured in Dulbecco's modified Eagle's medium containing 10% fetal calf serum.

30 Analysis of recombinant TNF α 55kD receptor derivatives

TNF α was radioiodinated with the Iodogen method (Pierce) according to the manufacturer's instructions. The specific activity of the ^{125}I -TNF α was 10-30 $\mu\text{Ci}/\mu\text{g}$. COS cells

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transfected with the TNF α receptor cDNA (pTNFR, 1300 bp EcoRI fragment) were incubated for 24 hours and then seeded into six well tissue culture plates (Nunc) at 4.5×10^8 cells per well. The cells were incubated for a further 48 hours and then receptor expression was quantitated by radioligand binding for 2 hours at 4°C. Non-specific binding of ^{125}I -TNF α was determined in the presence of a 1,000 fold molar excess of unlabelled TNF α . Binding data was analysed by the method of Scatchard (14).

10 The TNF α receptor derivative was analysed for inhibition of ^{125}I -TNF α binding to the natural receptor on human U937 cells. Culture supernatant was harvested 72 hours after COS cells were transfected with pTNFRcd. U937 cells (2×10^8 cells in 200 μl) were incubated with 1nM ^{125}I -TNF α and
15 dilutions of COS cell media for 2 hours at 4°C. Cells were then centrifuged through 20% sucrose to remove unbound TNF α . Non-specific binding was determined in the presence of 1 μM unlabelled TNF α .

The TNF α receptor derivative was also analyzed for
20 inhibition of TNF α cytotoxic effects in vitro. The cytotoxicity assay was performed as described on the TNF sensitive cell line WEHI 164 clone 13 (15). Serial dilutions of supernatants from COS cells transfected with pTNFRcd or mock transfected controls were incubated with a
25 constant amount of TNF α (1 ng/ml) for 1 hour at 27°C before addition to the assay.

2. RESULTS

Isolation and characterization of the TNF α 55kD receptor cDNA

30 A partial amino acid sequence of the TNF binding protein was used to design a synthetic oligonucleotide probe. The radiolabelled probe was used to screen a human placenta cDNA library in λ gdgt10 and ten hybridizing phage were isolated. The nucleotide and deduced amino acid sequences

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of the longest cDNA clone depicted in Figure 1. The third potential ATG initiation codon occurs at position 156 of the nucleotide sequence; the first two ATG codons are closely followed by termination codons, and the third ATG is preceded by the best translation initiation consensus nucleotides (16). The cDNA encodes an open reading frame of 1365 bases which codes for a polypeptide of 455 residues. Both of the peptide sequences determined by amino acid sequencing were identified in the encoded cDNA (17 of 19 and 18 of 19 matching residues). The amino terminal end identified for the TNF binding protein corresponds to the cDNA encoded sequence beginning at residue 41. The first 35 amino acids are generally quite hydrophobic and probably represent a signal sequence.

Residues 35-40 are highly charged (DREKR) and such a sequence is not typically found in secretory signal sequences (17); perhaps the natural receptor is processed by proteolysis after residue 40 which contains a dibasic cleavage site (KR). Hydropathy analysis of the protein sequence predicts a single transmembrane domain of 23 amino acids. This hydrophobic sequence divides the protein into an extracellular domain of 171 residues and a cytoplasmic domain of 221 residues. The amino acid composition determined for the TNF binding protein corresponds well with the predicted composition of the extracellular domain encoded by the cDNA (results not shown). The discrepancy between the predicted receptor size (40,000 daltons) and the size determined by SDS-polyacrylamide gel electrophoresis (65,000 daltons, 18-20) is probably due to glycosylation; there are four potential N-linked glycosylation sites in the sequence, three of which are in the extracellular domain. The sequence contains a large number (17) of cysteine residues, 24 of which are in the extracellular domain. The arrangement of these cysteine residues is similar to that of several other cell surface

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pr teins, suggesting that the TNF receptor is structurally related to a family of receptors.

A Northern blot analysis is presented in Figure 2. The ³²P-labelled cDNA hybridized to a single predominant band of oligo-dT selected RNA from human placenta or spleen. A minor larger transcript was also observed in RNA from a fibroblast cell line. The size of the hybridizing species is 2400 bases, in good agreement with the size of isolated cDNA. Also shown in Figure 2 is a Southern blot of human genomic DNA hybridized with a 600 bp probe from the cDNA. In each of the three different restriction digests, only a single hybridized signal was observed. Thus the TNF receptor that we have isolated appears to be encoded by a single gene.

15

Expression of recombinant TNF receptor sequences in mammalian cells

To confirm that the cDNA shown in Figure 1 indeed encodes the TNF receptor, the cDNA was engineered for expression in mammalian cells. The cDNA contains an EcoRI site at position 1270 of Figure 1. The receptor coding sequence was isolated as a 1300 bp EcoRI-fragment (containing all but the last 81 codons of the cytoplasmic domain) and inserted into a mammalian cell expression vector containing a cytomegalovirus promoter and SV40 transcription termination sequences (12). The resulting plasmid was transfected into COS cells which were analyzed for TNF receptor expression after three days. As shown in Figure 3, the transfected cells specifically bound radioiodinated TNF α in a saturable and dose dependent fashion. The population of COS cells expressed approximately 1×10^8 receptors per cell. The measured binding affinity of recombinant receptors was $2.5 \times 10^9 M^{-1}$ at 4°C which is in close agreement with natural receptor in human cells (19,20). The binding of ¹²⁵I-TNF α (1 nM) to

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th se c lls could b inhibit d by the addition f
unlabelled TNF α r lymphot xin (Figure 3b). COS cells
transfected with just the expression vector did not
significantly bind ^{125}I -TNF α (less than 2% of the binding
5 seen with the cDNA transfection).

The extracellular domain of the TNF receptor is
naturally shed from cells. To produce a similar
recombinant derivative, a stop codon preceding the
transmembrane domain was engineered into the cDNA by PCR
10 mutagenesis. The modified DNA was inserted into the
expression plasmid and subsequently transfected into COS
cells. After three days, the COS cell media was tested for
inhibition of TNF α binding to human U937 cells. As shown
in Figure 4a, the transfected cell media inhibited up to
15 70% of the binding of TNF α . The recombinant TNF receptor
derivative was next tested for inhibition of TNF α
biological activity. A sensitive bioassay for TNF α is a
measurement of cytotoxicity of mouse WEHI 164 (clone 13)
cells. The transfected cell media inhibited 60% of TNF α
20 cytotoxicity on this cell line (Figure 4b). Media from
mock transfected COS cells did not inhibit TNF α induced
cytotoxicity or binding. These experiments demonstrate
that the recombinant extracellular domain of the TNF
receptor is capable of binding TNF and inhibiting its
25 biological activity.

EXAMPLE 1: Expression of polypeptide consisting essentially
of the first three cysteine-rich subdomains of the
extracellular binding domain of the 55kD receptor

1. MATERIALS AND METHODS

30 Reagents

E. coli derived recombinant human TNF α had a specific
activity of 2×10^7 U/mg in an L929 cytotoxicity assay.
Oligonucleotides were purchased from Osw l DNA service
(University of Edinburgh).

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Generation of the recombinant soluble TNFR derivatives

Deletion of each of the subdomains in the recombinant soluble TNFR was achieved by means of PCR fragment joining and PCR mutagenesis. The sequence of the oligonucleotides used in these experiments is given in Table 1 and their locations relative to the four cysteine rich subdomains is shown in Figure 5. The four subdomains are lined up with respect to one another in Figure 6.

The plasmid pTNFRecd (Reference Example) is shown in Figure 7. pTNFRecd was further modified to remove 5' untranslated sequences by cloning of the Cla I/Bgl II digested product of a PCR using oligos 5' Cla and IIIA into ClaI/Bgl II digested pTNFRecd, to generate 5'-ΔCla. Digestion of 5'-ΔCla with Pst-I and religation resulted in the generation of pΔII, which lacks the second cysteine rich subdomain (Figure 9). The fourth cysteine rich subdomain was removed by cloning of the BglII/Hind III digested product of a PCR using oligonucleotides 5A and 4D into BglII/Hind III 5'-ΔCla; this introduced a termination codon after amino acid 167 (counting from the initial methionine) to yield pΔIV (Figure 11). The constructs p I (Figure 8) and pΔIII (Figure 10) which lack the first and third cysteine rich subdomains respectively were generated by joining PCR fragments by means of overlaps introduced into the primers used for the PCR. The gel purified products of PCR's using 5' Cla and IA and IB and 5D were mixed and subjected to further amplification using 5'Cla and 5D as primers. The resulting fragment was digested with ClaI and BglII and cloned into ClaI/BglII digested pTNFRecd, to yield pΔI.

Similarly the gel purified products of PCR's using 5' Cla and IIIA and IIIB and 5D were mixed and subjected to further amplification using 5'Cla and 5D as primers. This product was digested with BglII and HindIII and cloned into Bgl II/Hind III cut 5'-ΔCla to yield pΔIII. In all cases

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the cloned derivatives were analysed by restriction enzyme analysis and DNA sequencing using sequenase (United States Biochemical Corporation).

Table 1: Structure of the mutagenic oligonucleotides

5	Oligo	Sequence
	<u>Name</u>	
	5'Cla	5'-GTTCTATCGATAAGAGGCCATAGCTGTCTGGC-3'
	IA	5'-GCTCTCACACTCTCTCTTCTCCCTGTCCCCTAG-3'
	IB	5'-AGGGAGAAGAGAGAGTGTGAGAGCGGCTCCTTC-3'
10	IIIA	5'-TGCATGGCAGGTACACACGGTGTCCCGGTCCAC-3'
	IIIB	5'-GACACCGTGTGTACCTGCCATGCAGGTTTCTTT-3'
	4D	5'-GGCCAAGCTTCAGGTGCACACGGTGTTCCTG-3'
	5A	5'-GCTGCTCCAAATGCCGAAAG-3'
	5D	5'-AGTTCAAGCTTTACAGTGCCCTTAACATTCTAA-3'

15 Analysis of recombinant soluble TNFR derivatives

COS cells were maintained in Dulbecco's modified Eagles medium containing 5% foetal calf serum. The soluble TNF α receptor derivatives were transfected into monkey COS cells by means of lipofectin (GIBCO-BRL, Bethesda MD) according to the manufacturers protocol and cell free supernatants harvested 72 hours post transfection.

Inhibition of TNF α activity

The soluble TNF α receptor derivatives were analyzed for inhibition of TNF α cytotoxic activity in vitro. The cytotoxicity assay was performed as described on the TNF α sensitive cell line WEHI 164 clone 13. Serial dilutions of supernatants from COS cells transfected with the mutant receptors or mock transfected controls were incubated with a constant amount of TNF (1 ng/ml) for 1 hour at 37°C before addition to the assay.

2. RESULTS

In order to understand more about the contribution of

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th individual cysteine rich subdomains to th binding f
TNF α by the soluble form of the 55kD TNF receptor, we
removed each subdomain by PCR mutagenesis (Figure 5). COS
cells were transfected with each of these constructs and
5 the supernatants were assayed for their ability to inhibit
the cytotoxic activity of TNF α . Figure 12 panel A shows
that conditioned medium from COS cells tranfected with
pTNFRecd inhibits TNF α as previously described. Removal of
the fourth cysteine rich subdomain resulted in a protein
10 which, similar to TNFRecd, was a potent inhibitor of TNF α
(Figure 12 panel B). The mutants lacking the first, second
and third subdomains did not show any inhibitory activity
in the TNF α cytotoxicity assay.

EXAMPLE 2: Expression of polypeptide consisting essentially
15 of the first three cysteine-rich subdomains of the
extracellular binding domain of the 75kD receptor.

The coding region of the human 75kD TNF α receptor was
isolated from a T cell lambda ZAP library, using a probe
based on published sequences (3) and cloned into the EcoRI
20 site of a mammalian cell expression vector (12) resulting
in plasmid p75TNFR. In more detail, RNA was extracted from
a cell line expressing the 75kD receptor and reverse
transcribed. Any cell line expressing this receptor could
be used, such as those described by Smith et al (3). The
25 product of the reverse transcription was subjected to 25
cycles of PCR using the following primers:

5' CGC AGA ATT CCC CGC AGC CAT GGC GCC CGT CGC C 3'

and 5' GTA AGG ATC CTA TCG CCA GTG CTC CCT TCA GCT 3'.

These primers are directed against the extracellular
30 binding domain coding region of the 75kD receptor and were
taken from Smith et al (3). The amplified product was gel
purified and shown to encode TNFR. This was subsequently
us d to screen the library. Plaque purificati n was
performed ssentially as described in th Referenc Example

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exc pt that the probe was labelled by random priming (21) and hybridised in 50% formamid . Filters were washed in 0.2 x SSC (Standard Saline Citrate) twice at 60°C.

5 A derivative of the 75kD TNF α receptor was produced by engineering a termination codon just prior to the transmembrane domain. Referring to Figure 13, the polymerase chain reaction (PCR) technique was used to generate a 274 bp restriction fragment containing a BglII site at the 5' end and an Xba I site preceded by a TAG stop
10 codon at the 3' end. The PCR primers were 5' ACACGACTTCATCCACGGATA and 5'ACGTTCTAGACTAGTCGCCAGTGCTCCCTTCAGCTG. The PCR product was digested with Bgl II and Xba I, gel purified and cloned into the TNF receptor expression plasmid (described above)
15 digested with BglII and Xba I. DNA sequencing confirmed that the resulting plasmid contained the designed DNA sequence.

A similar approach was utilised to generate a construct which lacked the fourth cysteine-rich subdomain of the 75kD
20 TNF α receptor. PCR was performed using a primer upstream of the Esp I site in the 75kD TNFR and a primer which introduced a TAG termination codon and an Xba I site. The sequences of the primers was 5' CAG AAC CGC ATC TGC ACC TGC and 5'ACGTTCTAGACTTGACACACCAGTCTGATGTTTC respectively. The
25 PCR product was digested with EspI and Xba I and the 110bp DNA fragment gel purified and cloned into Esp I Xba I digested p75TNFR.

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CLAIMS

1. A polypeptide which is capable of binding human TNF α and which consists essentially of:

(a) the first three cysteine-rich subdomains, but not the
 5 fourth cysteine-rich subdomain, of the extracellular binding domain of the 55kD or 75kD receptor for human TNF α ; or

(b) an amino acid sequence having a homology of 90% or more with the said sequence (a).

10 2. A polypeptide according to claim 1, which consists essentially of the first three cysteine-rich subdomains of the extracellular binding domain of the 55kD receptor for human TNF α .

3. A polypeptide according to claim 2, which has the
 15 amino acid sequence: M G L S T V P D L L L P L
 V L L E L V G I Y P S G V I G L V P H L
 G D R E K R D S V C P Q G K Y I H P Q N
 N S I C C T K C H K G T Y L Y N D C P G
 P G Q D T D C R E C E S G S F T A S E N
 20 H L R H C L S C S K C R K E M G Q V E I
 S S C T V D R D T V C G C R K N Q Y R H
 Y W S E N L F Q C F N C S L C L N G T V
 H L S C Q E K Q N T V C T.

4. A DNA sequence which encodes a polypeptide as
 25 defined in any one of the preceding claims.

5. A DNA sequence according to claim 4, which comprises:

GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT
 TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT
 30 CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC
 TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC
 TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC
 ACA GTG GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC
 CGG CAT TAT TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC

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CTC TGC CTC AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG
AAC ACC GTG TGC.

6. A DNA sequence according to claim 4 or 5, which
further comprises a 5' sequence which encodes a signal
5 amino acid sequence.

7. A DNA sequence according to claim 4, which is:
ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCG CTG GTG CTC
CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG
GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT CCC
10 CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC
AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG
GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC
GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC
CGA AAG GAA ATG GGT CAG GTG GAG ATC TT TCT TGC ACA GTG GAC
15 CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT
TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC
AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG
TGC ACC.

8. A vector which incorporates a DNA sequence as
20 claimed in any one of claims 4 to 7 and which is capable,
when provided in a suitable host, of expressing the said
polypeptide.

9. A vector according to claim 8, which is a
plasmid.

25 10. A host transformed with a vector as claimed in
claim 8 or 9.

11. A host according to claim 10, which is a
mammalian cell line.

12. A process for the preparation of a polypeptide as
30 defined in claim 1, which process comprises culturing a
transformed host as claimed in claim 10 or 11 under such
conditions that the said polypeptide is expressed.

13. A pharmaceutical composition comprising a
pharmac utically acceptable carrier r dilu nt and, as an

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active principle, a polypeptide as claimed in claim 1.

14. A polypeptide as defined in claim 1 for use in the treatment of rheumatoid arthritis.

Fig. 1.

1	ACCA GTGATCTCTA TGCCGGAGTC TCAAACCCTCA ACTGTACACT CAAGGCACITT GGGACGTCTT GGACAGACCG
75	AGTCCCGGA AGCCCCAGCA CTGCCGCTGC CACACTGCCC TGAGCCCAA TGGGGAGTG AGAGGCCATA GCTGTCTGGC
40 M	G L S T V P D L L L P L V L L E L L V G I Y P
156	ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG COG CTG GTG CTC CTG GAG CTG TTG GTG ATA TAC CCC
16 S	G V I G L V P H L G D R E K R D S V C P Q G K
228	TCA GGG GTT ATT GGA CTG GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT CCC CAA GGA AAA
9 Y	I H P Q N N S I C C T K C H K G T Y L Y N D C
300	TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT
33 P	G P G Q D T D C R E C E S G S F T A S E N H L
372	CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC GCT TCA GAA AAC CAC CTC
57 R	H C L S C S K C R K E M G Q V E I S S C T V D
444	AGA CAC TGC CTC AGC TGC TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC
81 R	D T V C G C R K N Q Y R H Y W S E N L F Q C F
516	CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG AGT GAA AAC CTT TTC CAG TGC TTC
105 N	C S L C L N G T V H L S C Q E K Q N T V C T C
558	AAT TGC AGC CTC TGC CTC AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC TGC
129 H	A G F F L R E N E C V S C S N C K K S L E C T
660	CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT AGT AAC TGT AAG AAA AGC CTG GAG TGC ACG
153 K	L C L P Q I E N V K G T E D S G T T
732	AAG TTG TGC CTA CCC CAG ATT GAG AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC ACA GTG CTG TTG CCC CTG
177 V	I F F G L C L L S L L F I G L M Y
804	GTC ATT TTC TTT GGT CTT TGC CTT TTA TCC CTC CTC ATT TTC ATT GGT TTA ATG TAT CGC TAC CAA CGG TGG AAG
201 S	K L Y S I V C G K S T P E K E G E L E G T T T
876	TCC AAG CTC TAC TCC ATT GTT TGT GGT GGG AAA TCG ACA CCT GAA AAA GAG GGG GAG CTT GAA GGA ACT ACT ACT

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Fig. 1(cont.)

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225 K P L A P N P S F S P T P T P T L G F S P V
 948 AAG CCC CTG GCC CCA AAC CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC CCC ACC CTG GGC TTC AGT CCC GTG

249 P S S T F T S S S T Y T P P G D C P N F A A P R R
 1020 CCC AGT TCC ACC TTC ACC TCC AGC TCC AGC TAT ACC CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC CGC AGA

273 E V A P P Y Q G A D P I L A T A L A S D P I P N
 1092 GAG GTG GCA CCA CCC TAT CAG GGG GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC TCC GAC CCC ATC CCC AAC

297 P L Q K W E D S A H K P Q S L D T D P A T L Y
 1164 CCC CTT CAG AAG TGG GAG GAC AGT GCC CAC AAG CCA CAG AGC CTA GAC ACT GAT GAC CCC GCG AGC CTG TAC

321 A V V E N V P P L R T L E F V R R L G L S D H E
 1236 GCC GTG GTG GAG AAC GTG CCC CCG TTG CGC TGG AAG GAA TTC GTG CGG CGC CTA GGG CTG AGC GAC CAC GAG

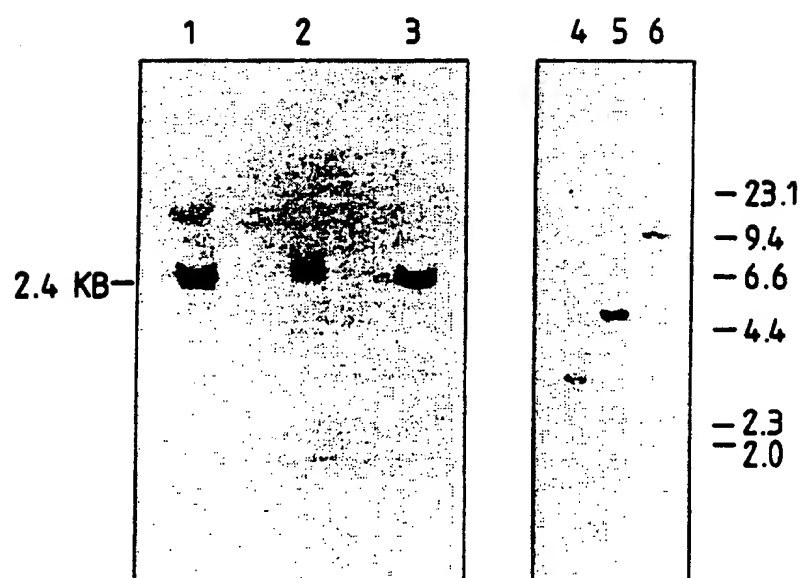
345 I D R L E L Q N G R C L R E A Q Y S M L A T W R
 1308 ATC GAT CGG CTG GAG CTG CAG AAC GGG CGC TGC CTG CGC GAG GCG CAA TAC AGC ATG CTG GCG ACC TGG AGG

369 R R T P R R CGG CGC GAG GCC ACG CTG GAG CTG GAG CTG GGA CGC GTG CTC CGC GAC ATG GAC CTG CTG GGC
 1380 CGG CGC ACG CCG CGG GAG GCC ACG CTG GAG CTG GAG CTG GGA CGC GTG CTC CGC GAC ATG GAC CTG CTG GGC

393 C L E D I E E A L C G P A A L P P A P S L L R
 1452 TGC CTG GAG GAC ATC GAG GAG GCG CTT TGC GGC CCC GCC GCG CTC CGC CCC AGT CTT CTC AGA TGA
 1521 GGCTGGCCCGC TGCGGGCAGC TCTAAGGACC GTCTCGCAG ATCGCCTTCC AACCCACCTT TTTTCTGGAA AGGAGGGGTC
 1601 CTGAGGGGC AAGCAGGAGC TAGCAGCCGC CTACTTGGTG CTAACCCCTC GATGTACATA GCTTTCTCA GCTGCTGCG
 1681 CGCGCCGAC AGTCAGCGCT GTGCGCGCG AGAGAGGTGC GCCGTGGGCT CAAGAGCCTG AGTGGGTGGT TTGCGAGGAT
 1761 GAGGGACGCT ATGCCTCATG CCGTFTTGG GTGTCTTCAC CAGCAAGGCT GCTCGGGGC CCCTGGTTCG TCCCTGAGCC
 1841 TTTTTCACAG TGCATAAGCA GTTTTFTT TTTTGTGTTT GTTTTGTGTTT TCAATCAATGT TACACTAATA
 1921 GAAACTTGGC ACTCCTGTGC CCTCTGCCCTG GACAAGCAG ATAGCAAGCT GAATGTCTT AAGGCAGGGG CGAGCACGGA
 2001 ACAATGGGGC CTTTCAGCTGG AGCTGTGGAC TTTTGTACAT ACATAAAAT TCTGAAGTTA AG

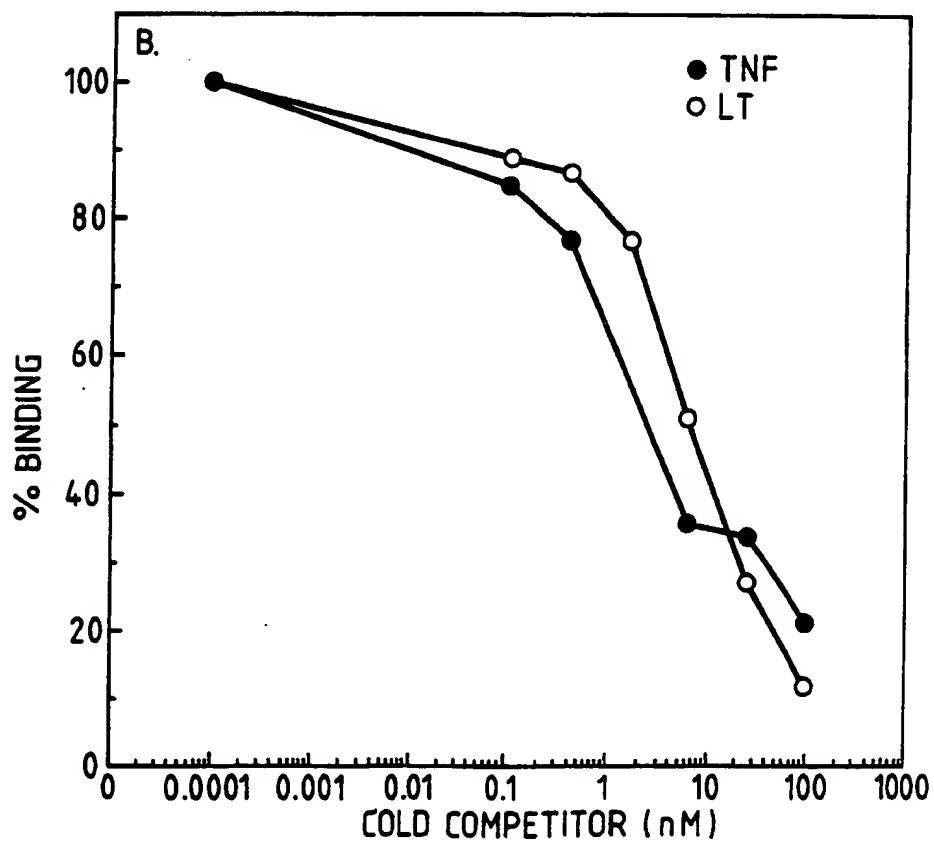
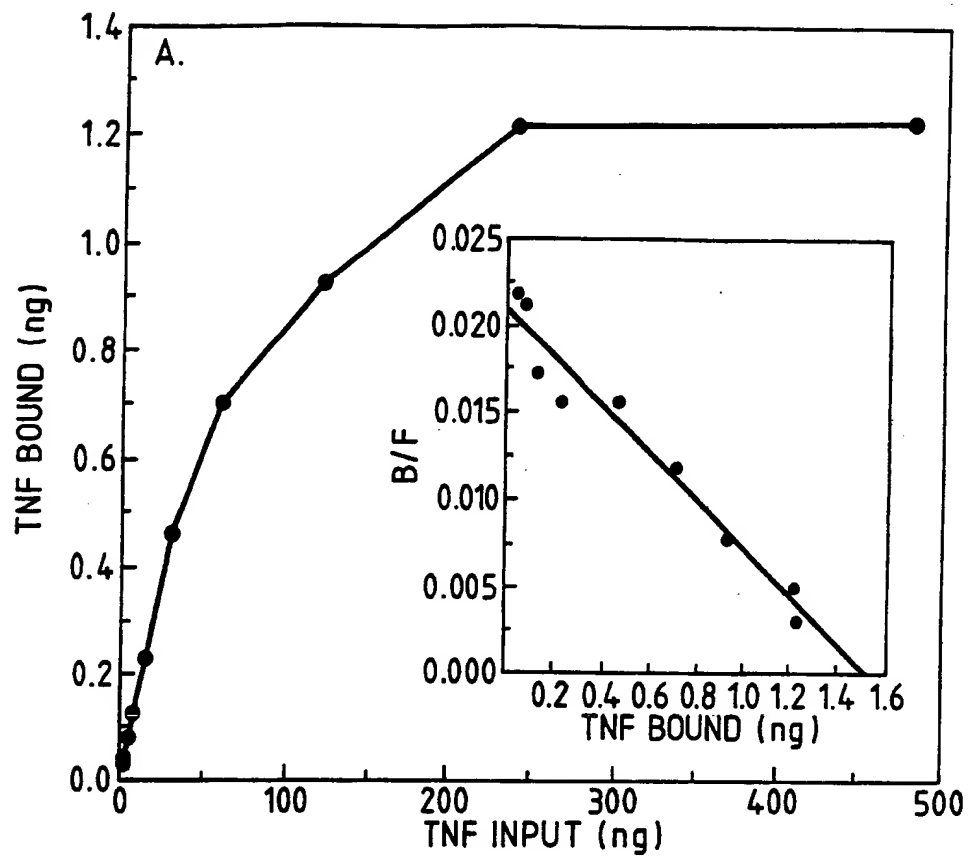
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Fig. 2.

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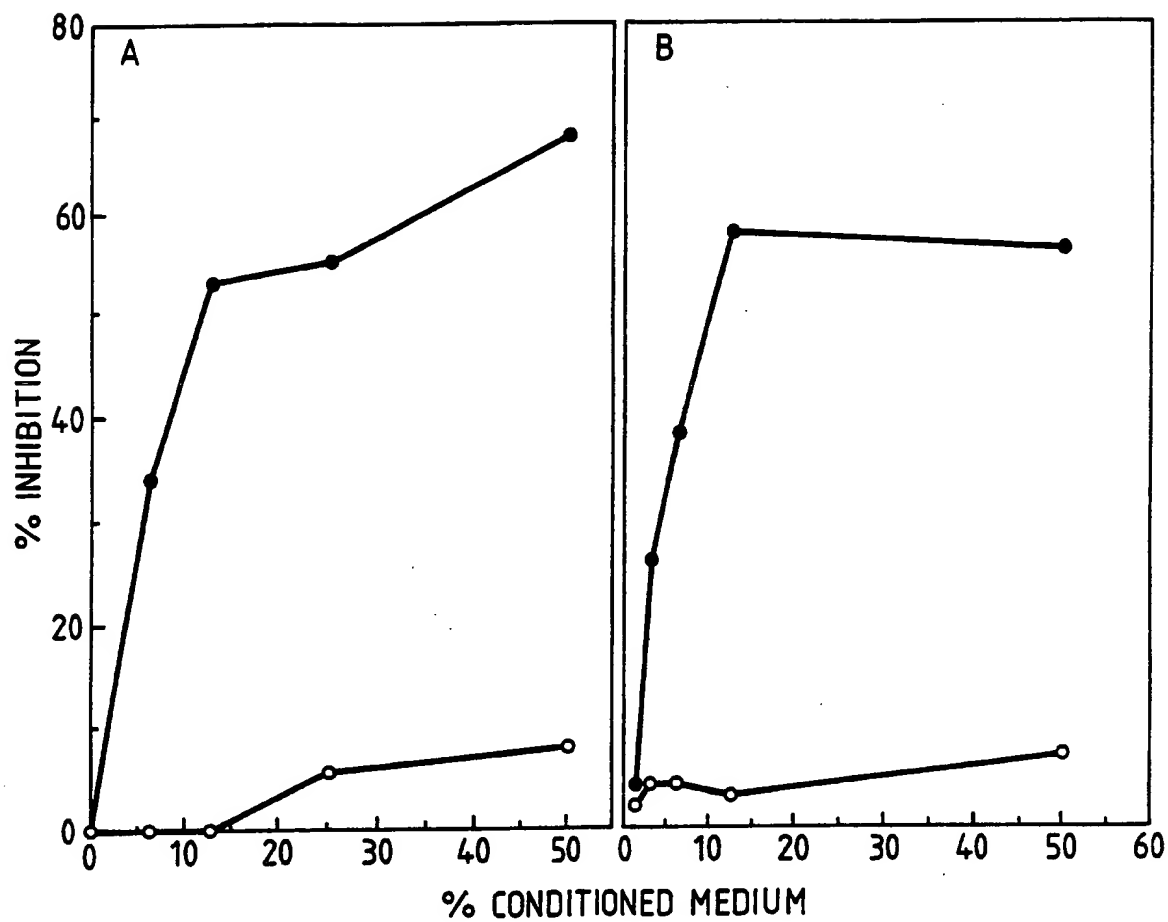
Fig. 3.



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Fig. 4.



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Fig. 5.

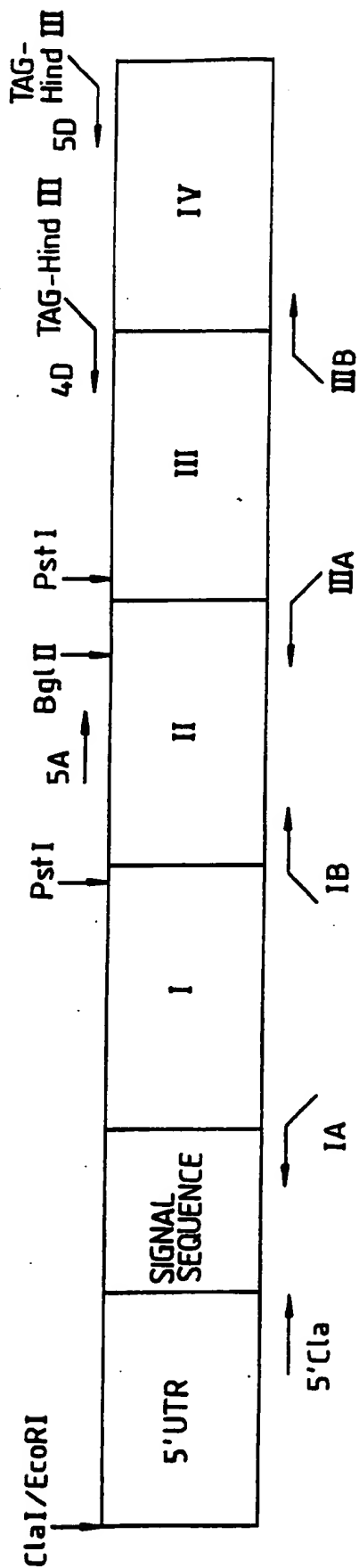
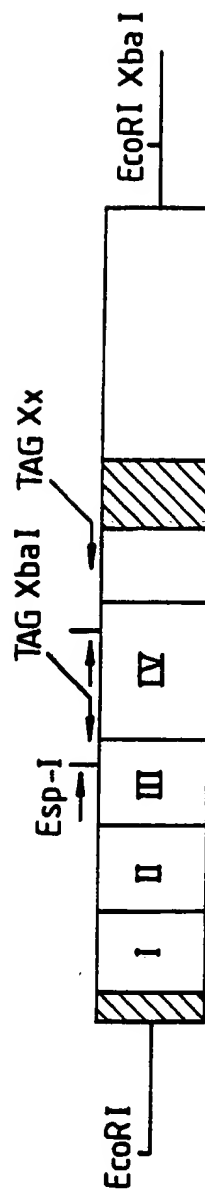


Fig. 13.



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Fig. 6.

First Subdomain

V C P Q G K Y I H P Q N S I G C I K C H K G T Y L Y N D C P G P G Q D T D C R
 T C R L R E Y Y D Q T A Q M C C S K C S P G Q H A K V F C T K T S D T V C D
 A C R E K Q Y L I S G E C C K A C N L G E G V A Q P C G A N Q T V C E
 N C V K D T Y P S G H K K C C R E C Q P G H G M V S R C D H T R D T V C H

Second Subdomain

E C E S G S F T A S E N H L R H C L S C S K R K E M G Q V E I S S C T V D R D T V C
 S C E D S T Y T Q L W N V P E C L S C G S R C S D Q V E T Q A C T I R E Q N R I C
 P C L D N V T F S D V V S A T V S A T T E C L G L Q S M S A P C V E A D A V C C
 P C G E S E F L D T W N R E T H C H Q H K Y C D P N H R S G S E L K Q N C T P T E D T V C
 P C E P G F Y N E A V N Y D T C K Q C T Q C N H R S G S E L K Q N C T P T E D T V C

Third Subdomain

G C R K N Q Y R H Y W S E N L F Q C F N C S L C L N G T V H L S C Q E K Q N T V C
 T C R P G W Y C A L S K Q E G C R L C A P L R K C R P G F G V A R P G T E T S D V V C K
 R C A Y G Y Y Q D E E T G H C E A C S V C E V G S G L V F S C Q D K Q N T V C E
 T C E E G W H C T S E A C E S C V L H R S C S P G F G V K Q I A T G V S D T I C E

Fourth Subdomain

T C H A G F F L R E N S T S T D I C R P H Q I C N V V A I P G N A S M D A V C T
 P C A P G T F S N T S S T D I C R P H Q I C N V V A I P G N A S M D A V C T
 E C P E G T Y S D E A N H V D P C C L P P C T V C E D T E R Q L R E C T P W A D A E C E
 P C P V G F F S N V S S A F E K C P W T N C T L S G K Q I R H P A S N S L D T V C G
 P C P P G H F S P G S N Q A C C K P W T N C T L S G K Q I R H P A S N S L D T V C E

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Fig. 7.

9	69	129	189	249	309	369	429	489	549	609	669	729	789	849	909	969	1029	1089	1149	1209	1269	1329	1389	1449	1509	1569	1629	1689	1749	1809	1869	1929	1989	2049	2109	2169	2229	2289	2349	2409	2469	2529	2589	2649	2709	2769	2829	2889	2949	3009	3069	3129	3189	3249	3309	3369	3429	3489	3549	3609	3669	3729	3789	3849	3909	3969	4029	4089	4149	4209	4269	4329	4389	4449	4509	4569	4629	4689	4749	4809	4869	4929	4989	5049	5109	5169	5229	5289	5349	5409	5469	5529	5589	5649	5709	5769	5829	5889	5949	6009	6069	6129	6189	6249	6309	6369	6429	6489	6549	6609	6669	6729	6789	6849	6909	6969	7029	7089	7149	7209	7269	7329	7389	7449	7509	7569	7629	7689	7749	7809	7869	7929	7989	8049	8109	8169	8229	8289	8349	8409	8469	8529	8589	8649	8709	8769	8829	8889	8949	9009	9069	9129	9189	9249	9309	9369	9429	9489	9549	9609	9669	9729	9789	9849	9909	9969	10029	10089	10149	10209	10269	10329	10389	10449	10509	10569	10629	10689	10749	10809	10869	10929	10989	11049	11109	11169	11229	11289	11349	11409	11469	11529	11589	11649	11709	11769	11829	11889	11949	12009	12069	12129	12189	12249	12309	12369	12429	12489	12549	12609	12669	12729	12789	12849	12909	12969	13029	13089	13149	13209	13269	13329	13389	13449	13509	13569	13629	13689	13749	13809	13869	13929	13989	14049	14109	14169	14229	14289	14349	14409	14469	14529	14589	14649	14709	14769	14829	14889	14949	15009	15069	15129	15189	15249	15309	15369	15429	15489	15549	15609	15669	15729	15789	15849	15909	15969	16029	16089	16149	16209	16269	16329	16389	16449	16509	16569	16629	16689	16749	16809	16869	16929	16989	17049	17109	17169	17229	17289	17349	17409	17469	17529	17589	17649	17709	17769	17829	17889	17949	18009	18069	18129	18189	18249	18309	18369	18429	18489	18549	18609	18669	18729	18789	18849	18909	18969	19029	19089	19149	19209	19269	19329	19389	19449	19509	19569	19629	19689	19749	19809	19869	19929	19989	20049	20109	20169	20229	20289	20349	20409	20469	20529	20589	20649	20709	20769	20829	20889	20949	21009	21069	21129	21189	21249	21309	21369	21429	21489	21549	21609	21669	21729	21789	21849	21909	21969	22029	22089	22149	22209	22269	22329	22389	22449	22509	22569	22629	22689	22749	22809	22869	22929	22989	23049	23109	23169	23229	23289	23349	23409	23469	23529	23589	23649	23709	23769	23829	23889	23949	24009	24069	24129	24189	24249	24309	24369	24429	24489	24549	24609	24669	24729	24789	24849	24909	24969	25029	25089	25149	25209	25269	25329	25389	25449	25509	25569
---	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

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Fig. 8.

DNA sequence	482 b.p.	TGTCCTGGCATGG ... CCCCAGATTAG	linear
9 / 1		39 / 11	
ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCG CTG CTG GAG CTG TTG GTG			
met gly leu ser thr val pro asp leu leu leu pro leu val leu leu leu val			
69 / 21		99 / 31	
GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA			
gly ile tyr pro ser gly val ile gly leu val pro his leu gly asp arg glu lys arg			
129 / 41		159 / 51	
GAG TGT GAG AGC GGC TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC			
glu cys glu ser gly ser phe thr ala ser glu asn his leu arg his cys leu ser cys			
189 / 61		219 / 71	
TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TGC ACA GTG GAC CGG GAC			
ser lys cys arg lys glu met gly gln val glu ile ser ser cys thr val asp arg asp			
249 / 81		279 / 91	
ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CCG CAT TAT TGG AGT GAA AAC CTT TTC CAG			
thr val cys gly cys arg lys asn gln tyr arg his tyr trp ser glu asn leu phe gln			
309 / 101		339 / 111	
TGC TTC AAT TGC AGC CTC TGC CTC AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG			
cys phe asn cys ser leu cys leu asn gly thr val his leu ser cys gln glu lys gln			
369 / 121		399 / 131	
AAC ACC GTG TGC ACC TGC CAT GCA GGT TTC TTC CTA AGA GAA AAC GAG TGT GTC TCC TGT			
asn thr val cys thr cys his ala gly phe leu arg glu asn glu cys val ser cys			
429 / 141		459 / 151	
AGT AAC TGT AAG AAA AGC CTG GAG TGC ACG AAG TTG TGC CTA CCC CAG ATT TAG			
ser asn cys lys lys ser leu glu cys thr lys leu cys leu pro gln ile AMB			

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Fig. 9.

DNA sequence	470 b.p.	TGCTGGCATGG ... CCCAGATTAG	linear
9 / 1		39 / 11	
ATG GGC CTC	TCC ACC GTG CCT GAC CTG CTG	CCG CTG	CTG GAG CTG TTG GTG
met gly leu ser thr val pro asp leu leu leu val			
69 / 21		99 / 31	
GGA ATA TAC	CCC TCA GGG GTT ATT GGA CTG GTC CCT CAC	CTA GGG GAC AGG GAG AAG AGA	
gly ile tyr pro ser gly val ile gly leu val pro his leu gly asp arg glu lys arg			
129 / 41		159 / 51	
GAT AGT GTG	TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT	TGC ATT TGC TGT ACC	
asp ser val cys pro gln gly lys tyr ile his pro gln asn ser ile cys cys thr			
189 / 61		219 / 71	
AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC	CCG CAG GAT ACG GAC		
lys cys his lys gly thr tyr leu tyr asn asp cys pro gly pro gly gln asp thr asp			
249 / 81		279 / 91	
TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG AGT GAA AAC CTT	TTC CAG TGC TTC AAT TGC		
cys arg lys asn gln tyr arg his tyr trp ser glu asn leu phe gln cys phe asn cys			
309 / 101		339 / 111	
AGC CTC TGC CTC AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG	AAA CAG AAC ACC GTG TGC		
ser leu cys leu asn gly thr val his leu ser cys gln glu lys gln asn thr val cys			
369 / 121		399 / 131	
AACC TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT	GTC TCC TGT AGT AAC TGT AAG		
thr cys his ala gly phe phe leu arg glu asn glu cys val ser cys ser asn cys lys			
429 / 141		459 / 151	
AAA AGC CTG GAG TGC ACG AAG TTG TGC CTA CCC CAG ATT TAG			
lys ser leu glu cys thr lys leu cys leu pro gln ile AMB			

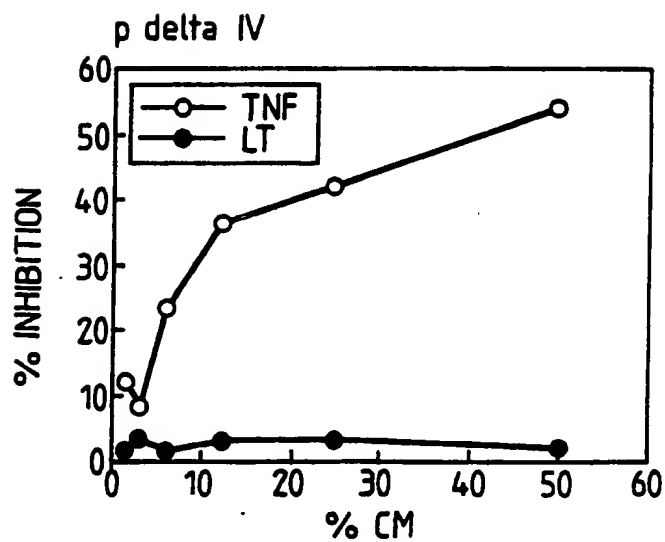
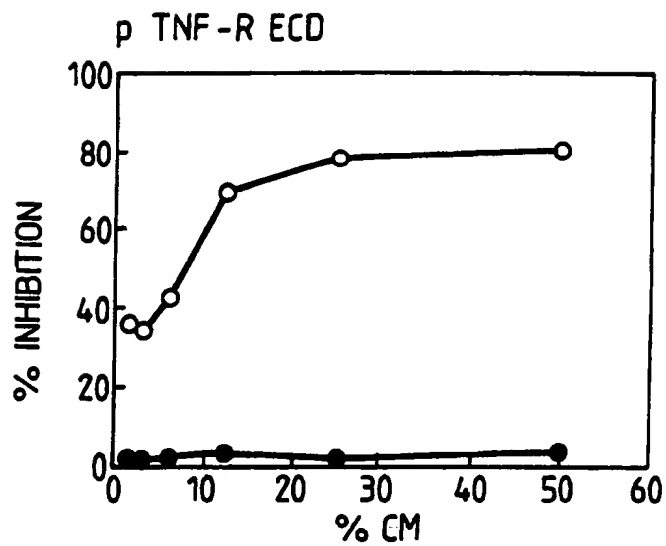
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Fig.10.

DNA sequence	485 b.p.	TGTCGCGCATGG ...	CCCCAGATTAG	linear
9 / 1		39 / 11		
ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CCG CTG CTG GAG CTG TTG GTG				
met gly leu ser thr val pro asp leu leu leu pro leu val leu leu leu val				
69 / 21		99 / 31		
GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA				
gly ile tyr pro ser gly val ile gly leu val pro his leu gly asp arg glu lys arg				
129 / 41		159 / 51		
GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC				
asp ser val cys pro gln gly lys tyr ile his pro gln asn ser ile cys cys thr				
189 / 61		219 / 71		
AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG CAG GAT ACG GAC				
lys cys his lys gly thr tyr leu tyr asn asp cys pro gly pro gly gln asp thr asp				
249 / 81		279 / 91		
TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC				
cys arg glu cys glu ser gly ser phe thr ala ser glu asn his leu arg his cys leu				
309 / 101		339 / 111		
AGC TGC TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC				
ser cys ser lys cys arg lys glu met gly gln val glu ile ser ser cys thr val asp				
369 / 121		399 / 131		
CGG GAC ACC GTG TGT ACC TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC TCC				
arg asp thr val cys thr cys his ala gly phe phe leu arg glu asn glu cys val ser				
429 / 141		459 / 151		
TGT AGT AAC TGT AAG AAA AGC CTG GAG TGC ACG AAG TTG TGC CTA CCC CAG ATT TAG				
cys ser asn cys lys lys ser leu glu cys thr lys leu cys leu pro gln ile AMB				

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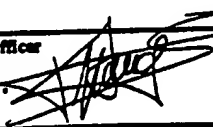
Fig.12.



INTERNATIONAL SEARCH REPORT

PCT/GB 91/01826

International Application No

I. CLASSIFICATION OF SUBJECT MATTER (If several classification symbols apply, indicate all) ⁶		
According to International Patent Classification (IPC) or to both National Classification and IPC Int.C1. 5 C12N15/12; C07K13/00; A61K37/02		
II. FIELDS SEARCHED		
Minimum Documentation Searched ⁷		
Classification System	Classification Symbols	
Int.C1. 5	C07K	
Documentation Searched other than Minimum Documentation to the Extent that such Documents are included in the Fields Searched ⁸		
III. DOCUMENTS CONSIDERED TO BE RELEVANT⁹		
Category ¹⁰	Citation of Document, ¹¹ with indication, where appropriate, of the relevant passages ¹²	Relevant to Claim No. ¹³
X	EP,A,0 308 378 (YEDA RESEARCH AND DEVELOPMENT COMPANY, LIMITED) 22 March 1989 see the whole document ---	1-14
X	CELL. vol. 61, 20 April 1990, CAMBRIDGE, NA US pages 351 - 359; Shall, T.J. et al.: 'Molecular cloning and expression of the human 55Kd tumor necrosis factor receptor.' see the whole document ---	1-14
X	CELL. vol. 61, 20 April 1990, CAMBRIDGE, NA US pages 361 - 370; Loetscher, H. et al.: 'Molecular cloning and expression of a receptor for human tumor necrosis factor.' see the whole document --- -/-	1-14
<p>¹⁰ Special categories of cited documents: ¹⁰</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier document but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.</p> <p>"A" document member of the same patent family</p>		
IV. CERTIFICATION		
Date of the Actual Completion of the International Search	Date of Mailing of this International Search Report	
23 JANUARY 1992	0 6. 02. 92	
International Searching Authority	Signature of Authorized Officer	
EUR PEAN PATENT OFFICE	NAUCHE S.A. 	

III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)		
Category *	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No.
X	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA. vol. 87, 1 October 1990, WASHINGTON US pages 7380 - 7384; Gray, Patrick W.; Barrett, Kathy; Chantry, David; Turner, Martin; Feldmann, Marc: 'Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant soluble TNF-binding protein' see the whole document ---	1-14
P,X	EP,A,0 393 438 (BOEHRINGER INGELHEIM INTERNATIONAL) 24 October 1990 see the whole document ---	1-14

**ANNEX TO THE INTERNATIONAL SEARCH REPORT
ON INTERNATIONAL PATENT APPLICATION NO. GB 9101826
SA 52300**

This annex lists the patent family members relating to the patent documents cited in the above-mentioned international search report.
The members are as contained in the European Patent Office EDP file on
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Patent document cited in search report	Publication date	Patent family member(s)	Publication date
EP-A-0308378	22-03-89	AU-A- 2206888 JP-A- 2000200	16-03-89 05-01-90

EP-A-0393438	24-10-90	DE-A- 3913101 DE-A- 3920282 JP-A- 3164179	31-10-90 03-01-91 16-07-91

FIG. 4A

	1	50
huCHD	MPSLPAPPAPLLLLGLLLGSRPARGAGPEPPVLP	IRSEKEPLPVRGAAG
huCHL	---MGGMKYIFSLIFFLLLEG-----	GKTEQVKHSETY
huCHL2	--MVPEYRVLSLLEGLALLWFP-----	LDSHARARPDME
	51	100
huCHD	CTFGGKVYALDETHWBDLGEPPFGVMRCVLCACEAPQWGRRTRG	PGRVRSCK
huCHL	CMFQDKKRYVGERWHPEYL-EPYGLVYCVNCICSENGNVLC	SR-----
huCHL2	CLFHGKRYSPGESWHPEYL-EPQGLMYCLRCTCSEGAHV	SCYR-----
	101	150
huCHD	NIKPECPPTPAGGQPRQLPGHCQTCPOERSSSERQPSGLSFEYPRD	PEHR
huCHL	---VRCPNVHCLSPVHPEHLCCPRCPEDSLPPV---	NKVTSKSCEYNG
huCHL2	---LHCBPVHCPOQVTEPQQCCPKVEPHTPSG----	LRAPPKSCOHNH
	151	200
huCHD	SYSDRGEPGAEEERARGDGHTDFVALLTGPRSQAVARARVSLLR	SSLRFSI
huCHL	TTYQHGEHFFVAEGLFQNRQPNQCTQCSCSEG-----	
huCHL2	TMYQHGEHFFSAHELFP SRLPNQCVCSCTEG-----	
	201	250
huCHD	SYRRDRPTRIRFSDSNGSVLFEHPAAPTQDGLVCGVWRAVPRL	SLRLLR
huCHL	-----NMVYGLKTCPKLTCAFPVSVYPDSCCRVCRGDG-	ELSW
huCHL2	-----QTYCGLTTCPEPCCPAPLPLPDSCCOACKDEASEQSD	
	251	300
huCHD	AEQLHVALVTITHTPSGEVWGPLIRHRLAAETFSAILLTLEGPP	QQGVGGI
huCHL	EHSDDGDI FROPANREARHSYHRSHYDPPPSRQAGGLSRFP-	
huCHL2	EEDSVQSLHGVRRHPQDPCSSDAGRKRGPCTPAPTGLS-	
	301	350
huCHD	TLLTSLDTEDSLHFLLLFRGLLEPRSGGLTOVPIRLQILHOGOL	RELOA
huCHL	-----GARSHRGALMBSQQASGTIVQIVINNKHKHGQVCV	SNG
huCHL2	-----APLSFIPRHFRPKGAGSTTVKIVLKEKHKK--	ACVHGG
	351	400
huCHD	NVSAQEPGEAEVLPNLTVOEMDWLVLGELQMALEWAGRPEGLRIS	GHIAR
huCHL	KTYSHGESWHPNLRAPGIVMECVLCTCNVTQOECKKTHCPNRY	PCKYPQKI
huCHL2	KTYSHGEVWHPAFRAFGPIPCILCTCEDGRQDCQRMTCPT	EYPCRHPKV
	401	450
huCHD	KSCDVLQSVLCGADALFVQTEGAAGSASLTLLGNGSLIYQVQV	VGTSSEV
huCHL	DGKCKKCPGKKAKEELPGQSFDNKG YFCGEETMPVYESVFMED	GETTRK
huCHL2	AGKCKKICP---EDKADPGHSEISSTRCPKAPGRVLVHTSVSP	SPDNLRR
	451	500
huCHD	VAMTLETKPQRRDQRTVLCHMAGLOPGGHTAVGICPGLGARGA	HMLONE
huCHL	IALETERPPQ-----MEVHWVWTRKG-----	ILQHF
huCHL2	FALEHEASDL-----MEVHWVWKLVKG-----	IFHLT

FIG. 4B

	501	550
huCHD	LFLNVGT ³ K ³ DFPD ¹ GELRGH ¹ VAAL ¹ PC ¹ GH ¹ SARHDTLPV ¹ PLAGALVLPPVKSQ	
huCHL	HIEK ¹ ISK ¹ R-MF ¹ EELPHFKLV ¹ TRTTLSQWKIFTEGEAQISQMCSSRVCRT ¹ E	
huCHL2	QIKKVRKQDFQKEAQHFRLLAGPHEGHWNVFLAQTL ¹ ELKVTASPDKVTKT	
	551	600
huCHD	AAGHAWLSLDTHCHLHYEVLLAGLGGSEQGTVTAHLLGPPGTPGPRRLK	
huCHL	LEDLVKVL ¹ YLERSEK ¹ HC-----	
huCHL2	-----	
	601	650
huCHD	GFYGSEAQGVVKDLEPELLRHLAKGMASLLITTKGSPRGELRGQVHIANQ	
huCHL	-----	
huCHL2	-----	
	651	700
huCHD	CEVGGLRLEAAGAEGVRALGAPDTASAAPPVVPGLPALAPAKPGGPGRPR	
huCHL	-----	
huCHL2	-----	
	701	750
huCHD	DPNTCFFEGQQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVCPPPSCPH	
huCHL	-----	
huCHL2	-----	
	751	800
huCHD	PVQAPDQCCPVCPEKQDVRDL ¹ PGLPRSRDPGEGCYFDGDRSWRAAGTRWH	
huCHL	-----	
huCHL2	-----	
	801	850
huCHD	PVVPPFGLIKCAVCTCKGGTGEVHCEKVQCPRLACAQPVVRVNPTDCCCKQC	
huCHL	-----	
huCHL2	-----	
	851	900
huCHD	PVGSGAHPQLGDPMQADGPRGCRFAGQWFPESQSWHPSVPPFGEMSCITC	
huCHL	-----	
huCHL2	-----	
	901	950
huCHD	RCGAGVPHCERDDCSLPLSCGSGKESRCCSRCTAHRRPAPETR ¹ TDPELEK	
huCHL	-----	
huCHL2	-----	
	951	
huCHD	EAEGS	
huCHL	-----	
huCHL2	-----	